

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:49:01 ; Search time 18.17 Seconds
(without alignments)
26.232 Million cell updates/sec

Title: US-09-432-546-4

Sequence: 1 RRMPPMPPMKWPLI 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	62	62.6	144 1	INDC_BOVIN
2	52	52.5	1112 1	ADRO_BOVIN
3	51.5	52.0	492 1	ADRO_BOVIN
4	51	51.5	1173 1	VG12_CVH22
5	50.5	51.0	278 1	RCEL_RHOGE
6	50.5	51.0	494 1	ADRO_RAT
7	49.5	50.0	253 1	Y945_MYCTU
8	49.5	50.0	491 1	ADRO_HUMAN
9	48.5	49.0	212 1	PR12_PIG
10	48.5	49.0	228 1	PR12_PIG
11	48	48.5	990 1	ENV_OMVVS
12	47	47.5	942 1	ENV_CAEVG
13	47	47.5	966 1	ENV_CAEVG
14	47	47.5	982 1	ENV_VILV
15	47	47.5	983 1	ENV_VILV
16	47	47.5	989 1	ENV_VILV
17	46	46.5	991 1	ENV_VILV
18	46	46.5	533 1	UBIB_PSEAB
19	46	46.5	572 1	GAG_IPHA
20	45.5	46.0	660 1	FGUB_ECOLI
21	45	45.5	115 1	NUPM_BOVIN
22	45	45.5	115 1	NUPM_BOVIN
23	45	45.5	115 1	NUPM_BOVIN
24	45	45.5	115 1	NUPM_BOVIN
25	45	45.5	115 1	NUPM_BOVIN
26	44	44.4	115 1	ACML_DROME
27	44	44.4	407 1	FUCO_CANFA
28	44	44.4	485 1	ADRO_BOVIN
29	44	44.4	488 1	ADRO_BOVIN
30	44	44.4	489 1	ADRO_BOVIN
31	44	44.4	492 1	ADRO_BOVIN
32	44	44.4	492 1	ADRO_BOVIN
33	44	44.4	492 1	ADRO_BOVIN

34	44	44.4	493 1	AERA_AERHY	P09167 aeromonas h
35	44	44.4	543 1	CP1B_RAT	O64678 ratius norv
36	44	44.4	655 1	HGFA_HUMAN	O04756 homo sapien
37	44	44.4	984 1	SG13_MOUSE	O04891 mus musculu
38	43.5	43.9	515 1	ENV_BLV	P51519 bovine leuk
39	43.5	43.9	515 1	ENV_BLVAF	P25504 bovine leuk
40	43.5	43.9	515 1	ENV_BLVAV	P25507 bovine leuk
41	43.5	43.9	515 1	ENV_BLVAV	P25505 bovine leuk
42	43.5	43.9	515 1	ENV_BLVAV	P25506 bovine leuk
43	43.5	43.9	515 1	ENV_BLVAV	P25507 bovine leuk
44	43.5	43.9	515 1	ENV_BLVAV	P03380 bovine leuk
45	43.5	43.9	515 1	ENV_BLVAV	P48300 canis fam11

ALIGNMENTS

RESULT	ID	INDC_BOVIN	STANDARD:	PRT:	144 AA.
AC	P33046	INDC_BOVIN	STANDARD:	PRT:	144 AA.
DT	01-OCT-1993	(Rel. 27, Created)			
DT	01-OCT-1993	(Rel. 27, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	INDOLICIDIN PRECURSOR.				
OS	Bos taurus (bovine)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RP	SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RC	MEDLINE=92393368; PubMed=1520337;				
RA	del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;				
RA	"CDNA Cloning of the neutrophil bactericidal peptide indolicidin.";				
RL	Biochem. Biophys. Res. Commun. 187:467-472(1992).				
RP	SEQUENCE OF 131-143.				
RC	TISSUE=Neutrophils;				
RA	Medline=92165771; PubMed=1537821;				
RA	Selsted M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W.,				
RA	Cullor J.S.;				
RT	"Indolicidin, a novel bactericidal tridecapeptide amide from				
RT	neutrophils.";				
RL	J. Biol. Chem. 267:4292-4295(1992).				
CC	-1- FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST				
CC	STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.				
CC	-1- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.				
CC	-1- PM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.				
CC	-1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.				
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CC	ENTITIES REQUIRES A LICENSE AGREEMENT (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: X67340; CAA47755.1; -				
DR	PIR: JCI222; JCI222.				
DR	PIR: A42387; A42387.				
DR	InterPro: IPR001894; Cathelicidin.				
DR	Pfam: PF00666; Cathelicidins; 1.				
DR	Prodom: PD001838; Cathelicidin; 1.				
DR	PROSITE: PS00946; CATHELICIDINS_1; 1.				
DR	PROSITE: PS00947; CATHELICIDINS_2; 1.				
KW	Antibiotic; Amidation; Signal.				
FT	STGNAL	1	29	POTENTIAL.	
FT	PROPEP	30	130		
FT	PEPTIDE	131	143	INDOLICIDIN.	
FT	MOD_RES	30	30	PYRROLIDONE CARBOXYLIC ACID (BY	

FT DISULFID 85 96 SIMILARITY.
 FT DISULFID 107 124 BY SIMILARITY.
 FT MOD.RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 144 AA, 16479 MW, E3B1CBHE55C09911 CRC64;

Query Match 62.6%; Score 62; DB 1; Length 144;
 Best Local Similarity 75.0%; Pred. No. 0.088;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 RWPMPMK 9
 DB 135 KWPMPMR 142

RESULT 2
 CN3B_HUMAN STANDARD; PRT: 1112 AA.
 AC Q1370; Q00639; Q14408;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B (EC 3.1.4.17) (CYCLIC
 GMP INHIBITED PHOSPHODIESTERASE B) (CGI-PDE.B) (CGIPDE1) (CGIP1).
 GN PDE3B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=rat;
 EX MEDLINE=97038690; PubMed=8884271;
 RA Miki T., Taira M., Hockman S., Shimada F., Lieman J., Napolitano M.,
 Ward D., Taira M., Makino H., Manganiello V.C.;
 RT "Characterization of the cDNA and gene encoding human PDE3B, the
 cGMP isoform of the human cyclic GMP-inhibited cyclic nucleotide
 phosphodiesterase family";
 RT Genomics 36:476-485(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97079687; PubMed=8921398;
 RA Leobert R.W., Winterpacht A., Seipel B., Zabel B.U.;
 RT "Molecular cloning and chromosomal assignment of the human homologue
 of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A) -- a gene
 involved in fat metabolism located at 11p15.1";
 RT Genomics 37:211-218(1996).
 RL [1]
 RN FUNCTION: MAY PLAY A ROLE IN FAT METABOLISM.
 CC -1 CATALYTIC ACTIVITY: GUANOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 CC GUANOSINE 5'-PHOSPHATE.
 CC -1 ENZYME REGULATION: INHIBITED BY CGMP.
 CC -1 SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
 CC -1 TISSUE SPECIFICITY: ABUNDANT IN ADIPOSE TISSUES.
 CC -1 SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: U38178; AAC50724.1; -
 CC EMBL: D50640; BAA09306.1; JOINED.
 CC EMBL: D50625; BAA09306.1; JOINED.
 CC EMBL: D50626; BAA09306.1; JOINED.
 CC EMBL: D50627; BAA09306.1; JOINED.
 CC EMBL: D50628; BAA09306.1; JOINED.
 CC EMBL: D50629; BAA09306.1; JOINED.
 CC EMBL: D50630; BAA09306.1; JOINED.

DR EMBL: D50631; BAA09306.1; JOINED.
 DR EMBL: D50632; BAA09306.1; JOINED.
 DR EMBL: D50633; BAA09306.1; JOINED.
 DR EMBL: D50634; BAA09306.1; JOINED.
 DR EMBL: D50635; BAA09306.1; JOINED.
 DR EMBL: D50637; BAA09306.1; JOINED.
 DR EMBL: D50638; BAA09306.1; JOINED.
 DR EMBL: D50639; BAA09306.1; JOINED.
 DR EMBL: X95520; CAA64774.1; -
 DR MIM: 602047; -
 DR InterPro: IPR003607; HDC.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF00233; PDEase; 1.
 DR SMART: SM00471; HDC; 1.
 DR PROSITE: PS00126; PDEASE_I; 1.
 KM Hydrolase; CGMP; Membrane.
 FT DOMAIN 1077 1080 POLY-GU.
 FT CONFLICT 84 84 D -> A (IN REF. 2).
 FT CONFLICT 87 87 A -> V (IN REF. 2).
 SQ SEQUENCE 1112 AA, 124376 MW, E5141C3DA12E9B0 CRC64;

Query Match 52.5%; Score 52; DB 1; Length 1112;
 Best Local Similarity 62.5%; Pred. No. 9.6;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 WPMMPMK 10
 DB 169 WQWMSMP 176

RESULT 3
 ADRO_BOVIN STANDARD; PRT: 492 AA.
 AC P08165;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR
 DE (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)
 DE REDUCTASE).
 GN FDXR OR ADXR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP MEDLINE=94177140; PubMed=8130767;
 RA Takata Y., Sagara Y., Kono A., Sekimizu K., Horiuchi T.;
 RT "Gene structure of bovine adrenodoxin reductase";
 RL Biol. Pharm. Bull. 16:1200-1206(1993).
 RN [2]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE=8198050; PubMed=3448086;
 RA Sagara Y., Takata Y., Miyata T., Hara T., Horiuchi T.;
 RT "Cloning and sequence analysis of adrenodoxin reductase cDNA from
 RT bovine adrenal cortex";
 RL J. Biochem. 102:1333-1336(1987).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87270696; PubMed=3038094;
 RA Nonaka Y., Murakami H., Yabusaki Y., Kuramitsu S., Kagamiyama H.,
 Yamano T., Okamoto M.;
 RT "Molecular cloning and sequence analysis of full-length cDNA for mRNA
 RT of adrenodoxin oxidoreductase from bovine adrenal cortex";
 RL Biochem. Biophys. Res. Commun. 145:1239-1247(1987).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Adrenal cortex;
 RC MEDLINE=89170752; PubMed=2924777;
 RX Hanukoglu I., Guttinger T.;

FT CARBOHYD 930 930 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1015 1015 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1037 1037 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1049 1049 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1061 1061 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1066 1066 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1076 1076 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1082 1082 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1096 1096 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1173 1173 AA; 128639 MW; B9CA9A41A796B3BD CRC64;
SQ SEQUENCE

Query Match 51.5%; Score 51; DB 1; Length 1173;
Best Local Similarity 71.4%; Pred: No. 13; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

OY 2 RMPWPM 8
111111
Db 1113 KMPWPM 1119

RESULT 5
RCBL_RHOGE STANDARD; PRT; 278 AA.
ID RCBL_RHOGE
AC P51760;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE REACTION CENTER PROTEIN L CHAIN (PHOTOSYNTHETIC REACTION CENTER L SUBUNIT).
DE SUBUNIT.
GN PUPL.
OS Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
OC Rudriyivax
OC NCBI_Taxid-28068;
ON NCB1
RX NCB1
RN SEQUENCE FROM N.A.
RP STRAIN-1144;
RX MEDLINE-94132007; PubMed-8300574;
RA Nishimura K.V.P., Matsura K., Ohshima S., Shimada K.;
RT "Primary structure and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rudriyivax gelatinosus";
RT J. Biol. Chem. 269:2477-2484(1994).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN-51;
RX MEDLINE-97033541; PubMed-8879238;
RA Ouchane S., Picaud M., Reiss-Husson F., Vernotte C., Astier C.;
RT "Development of gene transfer methods for Rudriyivax gelatinosus S1: construction, characterization and complementation of a puf operon deletion strain";
RT Mol. Gen. Genet. 252:379-385(1996).
RL [1]
CC -1- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER PROCESS OF PHOTOSYNTHESIS.
CC -1- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS, TWO BACTERIOPEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND THREE HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, M, AND H).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA / PSBD FAMILY.
CC -----
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CC -----
CC EMBL: D16822; BAA04100.1; -

DR EMBL: U30310; AAA73927.1; -
DR EMBL: U51298; ABA1576.1; -
DR HSSP: P02934; 2RCR
DR InterPro: IPR000484; Photo_RC.
DR Pfam: PF00124; PhotocRC.1
DR PRINTS: PR00256; REACTIONCENTRE.
DR PRODOM: PD000551; Photo_RC.1.
DR PROSITE: PS00244; REACTION_CENTER; 1.
DR Transmembrane: Electron transport; Photosynthesis; Reaction center;
KW Iron; Magnesium.
FT INIT_MET 0 BY SIMILARITY.
FT TRANSSEM 32 POTENTIAL.
FT TRANSSEM 84 POTENTIAL.
FT TRANSSEM 112 POTENTIAL.
FT TRANSSEM 115 POTENTIAL.
FT TRANSSEM 170 POTENTIAL.
FT TRANSSEM 225 POTENTIAL.
FT METAL 173 POTENTIAL.
FT METAL 190 POTENTIAL.
FT METAL 230 POTENTIAL.
FT BINDING 216 POTENTIAL.
FT CONFLICT 278 POTENTIAL.
SQ SEQUENCE 278 AA; 31210 MW; 0ACFC1241890DC5 CRC64;

Query Match 51.0%; Score 50.5; DB 1; Length 278;
Best Local Similarity 42.9%; Pred: No. 4.3; Indels 9; Gaps 2;
Matches 9; Conservative 1; Mismatches 2;

OY 1 RMPWPM-----KMP 12
111111
Db 257 RGPWPMWMLNLPINSONPL 277

RESULT 6
ADRO_RAT STANDARD; PRT; 494 AA.
ID ADRO_RAT
AC P56522;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)-REDUCTASE).
DE PDXR
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_Taxid-10116;
ON NCB1
RN SEQUENCE FROM N.A., AND SEQUENCE OF 34-54.
RP STRAIN-NISTAR; TISSUE-Adrenal gland;
RX MEDLINE-99454627; PubMed-10525147;
RA Sagara Y., Watanabe Y., Kodama H., Aramaki H.;
RT "cDNA cloning, overproduction and characterization of rat adrenodoxin reductase";
RT Biochim. Biophys. Acta 1434:284-295(1999).
RL [1]
CC -1- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE MITOCHONDRIAL P450 SYSTEMS, INCLUDING CHOLESTEROL SIDE CHAIN CLEAVAGE IN ALL STEROIDGENIC TISSUES, STEROID 11-BETA HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24 HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE LIVER.
CC -1- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED ADRENODOXIN + NADPH.
CC -1- COFACTOR: FAD.
CC -1- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -----
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DR EMBL: D63761; BAA23759.1; -
 DR InterPro: IPR000759; Adnrx_redctse.
 DR PRINTS: PR00419; ADXRDYASE.
 KM Electron transport; Oxidoreductase; Flavoprotein; NADP: FAD;
 KM Mitochondrion; Transit peptide.
 FT TRANSIT 1 34
 FT CHAIN 35 494
 FT CHAIN 35 494
 SEQUENCE 494 AA; 54362 MW; 5F07B37DFAA9525D CRC64;

Query Match 51.0%; Score 50.5; DB 1; Length 494;
 Best Local Similarity 58.3%; Pred. No. 7.2;
 Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 RRMPMPMK-WP 11
 Db 4 RCRWMSWAMP 15

RESULT 7
 ID Y945_MYCTU STANDARD; PRT; 253 AA.
 AC P1564;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PUTATIVE OXIDOREDUCTASE RV0945 (EC 1.-.-.-).
 GN RV0945 OR MT0971 OR MTCY10D7.29C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_Taxid=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekela F.,
 RA Davies K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Haynes R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares R., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 (2)

RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Ormazabal L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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DR EMBL: Z79700; CAB02005.1; -
 DR EMBL: AE006982; AAK45219.1; -
 DR TIGR: MT0971; -
 DR Tuberculin; RV0945; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Hypothetical protein; Oxidoreductase; Complete proteome.
 FT ACT SITE 159 159
 FT ACT SITE 159 159
 SEQUENCE 253 AA; 27138 MW; BAD937208842DA12 CRC64;

Query Match 50.0%; Score 49.5; DB 1; Length 253;
 Best Local Similarity 70.0%; Pred. No. 5.3;
 Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 4 PWWPMPKPLI 13
 Db 230 PWWPMA-PLV 238

RESULT 8
 ID ADRO_HUMAN STANDARD; PRT; 491 AA.
 AC P2570; Q13716;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR
 DE (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)
 DE REDUCTASE)
 GN FDXR OR ADXR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89017146; PubMed=2845396;
 RA Solish S.B., Picado-Leonard J., Morel Y., Kuhn R.W., Mohandas T.K.,
 RA Hankoglu I., Miller W.L.;
 RT "Human adrenodoxin reductase: two mRNAs encoded by a single gene on
 RT chromosome 17cen-7q25 are expressed in steroidogenic tissues."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7104-7108(1988).
 (2)

RP SEQUENCE FROM N.A.
 RC MEDLINE=91046028; PubMed=2236061;
 RA Lin D., Shi Y., Miller W.L.;
 RT "Cloning and sequence of the human adrenodoxin reductase gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8516-8520(1990).
 CC -1- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE
 CC MITOCHONDRIAL P450 SYSTEMS, INCLUDING CHOLESTEROL SIDE CHAIN
 CC CLEAVAGE IN ALL STEROID-GENIC TISSUES, STEROID 11-BETA
 CC HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24
 CC HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE
 CC LIVER.
 CC -1- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED
 CC ADRENODOXIN + NADPH.
 CC -1- COFACTOR: FAD.
 CC -1- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC LONG FORM: ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
 CC REPRESENTS 10-20% OF ALL ADRENODOXIN REDUCTASE mRNA. AND SEEMS TO
 CC BE INACTIVE.

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CC -----
 DR EMBL; X75438; CAA53188.1; -;
 DR EMBL; X89202; CAA61488.1; -;
 DR InterPro: IPR001894; Cathelicidin.
 DR Pfam: PF00666; Cathelicidins; 1.
 DR ProDom: PD001838; Cathelicidin_1; 1.
 DR PROSITE: PS00946; CATHELICIDINS_1; 1.
 DR PROSITE: PS00947; CATHELICIDINS_2; 1.
 KW Antibiotic; Repeat; Amidation; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 146
 FT PEPTIDE 147 225
 FT PROPEP 226 228
 FT MOD_RES 225 225
 FT DOMAIN 132 228
 FT DOMAIN 148 217
 FT REPEAT 148 157
 FT REPEAT 158 167
 FT REPEAT 168 177
 FT REPEAT 178 187
 FT REPEAT 188 197
 FT REPEAT 198 207
 FT REPEAT 208 217
 FT MOD_RES 30 30
 FT DISULFID 85 96
 FT DISULFID 107 124
 SQ SEQUENCE 228 AA; 25855 MW; 1EA4511FE35CC182 CRC64;

Query Match 49.08; Score 48.5; DB 1; Length 228;
 Best Local Similarity 53.88; Pred. No. 6.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

OY 1 RRMPMPMKWPLI 13
 DB 129 RRPFW--WPFL 138

RESULT 11
 ENV_OMVVS STANDARD; PRT; 990 AA.
 AC P16899;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN).
 GN ENV.
 OS Ovine lentivirus (strain SA-OMV).
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11664;
 RX MEDLINE=90233989; PubMed=2158181;
 RA Querat G., Audoly G., Sonigo P., Vigne R.;
 RT "Nucleotide sequence analysis of SA-OMV, a visna-related ovine
 RT lentivirus: phylogenetic history of lentiviruses."; <http://www.isb-sib.ch/announce/>
 RT Virology 175:434-447(1990).
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CC -----
 DR EMBL; M34193; AAA46783.1; -;
 DR EMBL; M31646; AAA68817.1; -;
 DR PIR; G46335; G46335.
 DR HIV; M34193; ENV5OMV5ACG.
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; GP41; 1.
 KW Glycoprotein; Coat protein; Polypeptide; Transmembrane.
 FT PEPTIDE 1 101
 FT CHAIN 102 662
 FT CHAIN 663 990
 FT TRANSMEM 842 863
 FT CARBOHYD 141 141
 FT CARBOHYD 162 162
 FT CARBOHYD 207 207
 FT CARBOHYD 259 259
 FT CARBOHYD 299 299
 FT CARBOHYD 363 363
 FT CARBOHYD 386 386
 FT CARBOHYD 402 402
 FT CARBOHYD 413 413
 FT CARBOHYD 434 434
 FT CARBOHYD 438 438
 FT CARBOHYD 469 469
 FT CARBOHYD 474 474
 FT CARBOHYD 480 480
 FT CARBOHYD 490 480
 FT CARBOHYD 500 500
 FT CARBOHYD 514 514
 FT CARBOHYD 516 516
 FT CARBOHYD 526 526
 FT CARBOHYD 536 536
 FT CARBOHYD 542 542
 FT CARBOHYD 550 550
 FT CARBOHYD 560 560
 FT CARBOHYD 567 567
 FT CARBOHYD 703 703
 FT CARBOHYD 771 771
 FT CARBOHYD 778 778
 FT CARBOHYD 794 794
 SQ SEQUENCE 990 AA; 114498 MW; 279B816B55614F3 CRC64;

Query Match 48.5%; Score 48; DB 1; Length 990;
 Best Local Similarity 50.08; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 RRMPMPMKWPL 12
 DB 174 QEPWMTYHWP 185

RESULT 12
 ENV_CAEGV STANDARD; PRT; 942 AA.
 AC P31627;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: SURFACE
 DE PROTEIN, TRANSMEMBRANE PROTEIN].
 GN ENV.
 OS Caprine arthritis encephalitis virus (strain 663) (CAEV).
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11662;
 RX MEDLINE=92015464; PubMed=1656067;
 RA Harwood W.G., Stem T.A.;
 RT "Structure and genetic variability of envelope glycoproteins of two
 RT antigenic variants of caprine arthritis-encephalitis lentivirus."; <http://www.isb-sib.ch/announce/>
 RT J. Virol. 65:5744-5750(1991).
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ID	ENV_VILV	STANDARD:	PRT:	982 AA.
AC	P03379;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN).			
GN	ENV.			
OS	Visna lentivirus (strain 1514).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_Taxid=11742;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8554938; PubMed=2410140;			
RA	Sonigo P., Alizon M., Staekus K., Klatzmann D., Cole S., Danos O.,			
RA	Rezel E., Tioillais P., Haase A., Wain-Hobson S.;			
RT	"Nucleotide sequence of the visna lentivirus: relationship to the			
RT	AIDS virus.";			
RL	Cell 42:369-382(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86062965; PubMed=2824836;			
RA	Braun M.J., Clements J.E., Gonda M.A.;			
RT	"The visna virus genome: evidence for a hypervariable site in the env			
RT	gene and sequence homology among lentivirus envelope proteins.";			
Rb	J. Virol. 61:4046-4054(1987).			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M10608; -; NOT_ANNOTATED_CDS.			
DR	EMBL; M51543; -; NOT_ANNOTATED_CDS.			
DR	EMBL; A15114; CAA01216.1; -;			
DR	PIR; A03977; VCLJVS.			
DR	HIV; M10608; ENVSVLVCG.			
DR	InterPro; IPRO00328; Env_GP41.			
DR	Pfam; PF00517; GP41; 1.			
KM	Glycoprotein; Coat protein; Polypeptide; Transmembrane.			
FT	PEPTIDE	1	100	LEADER PEPTIDE.
FT	CHAIN	101	656	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	657	982	TRANSMEMBRANE GLYCOPROTEIN.
FT	TRANSMEM	835	851	POTENTIAL.
FT	CARBOHYD	140	140	
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	364	364	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	370	370	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	381	381	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	403	403	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	414	414	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	435	435	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	470	470	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	475	475	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	481	481	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	491	491	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	515	515	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	527	527	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	537	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>542<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	542 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>543<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	543 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>568<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	568 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>697<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	697 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>764<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	764 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>771<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	771 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>787<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	787 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>821<th>N-LINKED (GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	821 <th>N-LINKED (GLCNAC. . .)</th> <th>(POTENTIAL)</th>	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	VARIANT <td>12<th>T -> M (IN REF. 2).</th><th>(POTENTIAL)</th></td>	12 <th>T -> M (IN REF. 2).</th> <th>(POTENTIAL)</th>	T -> M (IN REF. 2).	(POTENTIAL)
FT	VARIANT <td>118<th>S -> N (IN REF. 2).</th><th>(POTENTIAL)</th></td>	118 <th>S -> N (IN REF. 2).</th> <th>(POTENTIAL)</th>	S -> N (IN REF. 2).	(POTENTIAL)
FT	VARIANT <td>283<th>K -> R (IN REF. 2).</th><th>(POTENTIAL)</th></td>	283 <th>K -> R (IN REF. 2).</th> <th>(POTENTIAL)</th>	K -> R (IN REF. 2).	(POTENTIAL)
FT	VARIANT <td>640<th>ER -> AQ (IN REF. 2).</th><th>(POTENTIAL)</th></td>	640 <th>ER -> AQ (IN REF. 2).</th> <th>(POTENTIAL)</th>	ER -> AQ (IN REF. 2).	(POTENTIAL)
FT	VARIANT <td>645<th>R -> K (IN REF. 2).</th><th>(POTENTIAL)</th></td>	645 <th>R -> K (IN REF. 2).</th> <th>(POTENTIAL)</th>	R -> K (IN REF. 2).	(POTENTIAL)
FT	SEQUENCE <td>982 AA; 113978 MW; 7D7BBA6E22BF53F CRC64;</td> <td></td> <td></td>	982 AA; 113978 MW; 7D7BBA6E22BF53F CRC64;		
QY	3 WPMWPKMPL 12			
Db	175 WPMNTYHMP 184			
RESULT 15				
ENV_VILVK	STANDARD;	PRT; 983 AA.		
ID	ENV_VILVK			
AC	P35954;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN).			
GN	ENV.			
OS	Visna lentivirus (strain KY1772).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=36374;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93174981; PubMed=8382414;			
RA	Andresson O.S., Elser J.E., Tobin G.J., Greenwood J.D., Gonda M.A.,			
RA	Georgsson G., Rattasdottilir V., Benediktssdottilir E., Carlsdottilir H.M.,			
RA	Maenlyla E.O., Rafnar B., Paltsson P.A., Casey J.W., Petursson G.;			
RT	Proteomic sequence and biological properties of a pathogenic			
RT	novel molecular clone of neurovirulent visna virus.";			
RL	Virology 193:89-105(1993).			
CC				
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CC	-----			
DR	EMBL; S55323; AAB25463.1; -			
DR	EMBL; L06906; AAA48362.1; -			
DR	PIR; E45390; E45390.			
DR	InterPro; IPR000328; Env_GP41.			
DR	PIR; P00517; GP41; 1.			
CC	Glycoprotein; Coat protein; Polyprotein; Transmembrane.			
KW	Glycoprotein; Coat protein; Polyprotein; Transmembrane.			
FT	PEPTIDE	1	LEADER PEPTIDE.	
FT	CHAIN	101	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	657	TRANSMEMBRANE GLYCOPROTEIN.	
FT	TRANSMEM	836	POTENTIAL.	
FT	CARBOHYD	140	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	161	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	206	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	258	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	298	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	364	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	381	N-LINKED (GLCNAC. . .)	(POTENTIAL)

FT CAROHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 470 470 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 765 765 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 788 788 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 822 822 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 900 900 R -> H (IN REF. 1; AAA48362).
SQ SEQUENCE 983 AA; 113939 MM; E03BCC254EA78268 CRC64;

Query Match 47.5%; Score 47; DB 1; Length 983;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 WPWMPKMWPL 12
111 : 111
Db 175 WPWMTYHMP 184

Search completed: January 30, 2002, 11:52:22
Job time: 201 sec